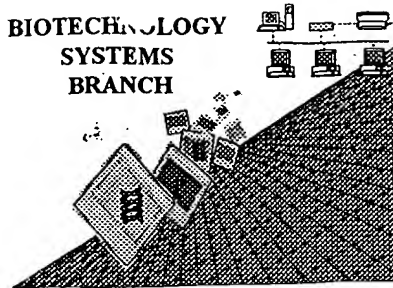


RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/881,457
Source: OIPK
Date Processed by STIC: 7/5/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/88/457

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
 Wrapped Aminos was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
 prevent "wrapping."

- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

- 3 Misaligned Amino The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
 Numbering use space characters, instead.

- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
 ensure your subsequent submission is saved in ASCII text.

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules,
 each n or Xaa can only represent a single residue. Please present the maximum number of each
 residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
 "bug" sequences(s) . Normally, PatentIn would automatically generate this section from the
 previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
 the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
 Artificial or Unknown sequences.

- 7 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

- 8 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (NEW RULES) <210> sequence id number
 <400> sequence id number
 000

- 9 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
 (NEW RULES) Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

- 10 Invalid <213> Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
 Response scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
 is Artificial Sequence

- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
 "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

- 12 PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
 "bug" resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
 listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING

DATE: 07/05/2001

PATENT APPLICATION: US/09/881,457

TIME: 11:30:02

Input Set : A:\SY01105K1QKQK Sequence Listing.txt

Output Set: N:\CRF3\07052001\I881457.raw

Does Not Comply
Corrected Diskette Needed*see
P. 3, too*

OK 3 <110> APPLICANT: Cochran, Mark D
 4 Cook, Stephanie M
 5 Wild, Martha A
 7 <120> TITLE OF INVENTION: Novel Avian Herpes Virus and Uses Thereof
 9 <130> FILE REFERENCE: SY01105K1QKQK
 11 <140> CURRENT APPLICATION NUMBER: US/09/881,457
 12 <141> CURRENT FILING DATE: 2001-06-14
 14 <150> PRIOR APPLICATION NUMBER: 09/426,352
 15 <151> PRIOR FILING DATE: 1999-10-25
 17 <150> PRIOR APPLICATION NUMBER: 08/804,372
 18 <151> PRIOR FILING DATE: 1997-02-21
 20 <150> PRIOR APPLICATION NUMBER: PCT/US95/10245
 21 <151> PRIOR FILING DATE: 1995-08-09
 23 <150> PRIOR APPLICATION NUMBER: 08/663,566
 24 <151> PRIOR FILING DATE: 1996-06-13
 26 <150> PRIOR APPLICATION NUMBER: 08/288,065
 27 <151> PRIOR FILING DATE: 1994-08-09
 29 <150> PRIOR APPLICATION NUMBER: PCT/US93/05681
 30 <151> PRIOR FILING DATE: 1993-06-14
 32 <150> PRIOR APPLICATION NUMBER: 08/023,610
 33 <151> PRIOR FILING DATE: 1993-02-26
 35 <150> PRIOR APPLICATION NUMBER: 07/898,087
 36 <151> PRIOR FILING DATE: 1992-06-12
 38 <160> NUMBER OF SEQ ID NOS: 5
 40 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

262 <210> SEQ ID NO: 2
 263 <211> LENGTH: 564
 264 <212> TYPE: PRT
 265 <213> ORGANISM: Newcastle disease virus
 267 <400> SEQUENCE: 2
 268 Met Asp Arg Ser Arg Leu Ala Pro Ser Arg Cys Arg Met Gly Ser Arg
 269 1 5 10 15
 271 Pro Ser Thr Lys Asn Pro Ala Pro Met Leu Thr Ile Arg Val Ala
 272 20 25 30
 274 Leu Val Leu Ser Cys Ile Cys Pro Ala Asn Ser Ile Asp Gly Arg Pro
 275 35 40 45
 E--> 277 Leu Ala Ala Ala Gly Xaa Trp Leu Gln Glu Thr Lys Gln Ser Thr Tyr
 278 50 55 60
 280 Thr Pro His Pro Arg Gln Val Asn His Ile Lys Leu Leu Pro Asn Leu
 281 65 70 75 80
 283 Pro Lys Asp Lys Glu Ala Cys Ala Lys Ala Pro Leu Asp Ala Tyr Asn
 284 85 90 95
 286 Arg Thr Leu Thr Thr Leu Leu Thr Pro Leu Gly Asp Ser Ile Arg Arg

*see
item 9
on Error
summary
sheet*

RAW SEQUENCE LISTING

DATE: 07/05/2001

PATENT APPLICATION: US/09/881,457

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Input Set : A:\SY01105K1QKQK Sequence Listing.txt

Output Set: N:\CRF3\07052001\I881457.raw

```

287          100          105          110
289 Ile Gln Glu Ser Val Thr Thr Ser Gly Gly Gly Arg Gln Gly Arg Leu
290          115          120          125
292 Ile Gly Ala Ile Ile Gly Gly Val Ala Leu Gly Val Ala Thr Ala Ala
293          130          135          140
295 Gln Ile Thr Ala Ala Ala Ala Leu Ile Gln Ala Lys Gln Asn Ala Ala
296 145          150          155          160
298 Asn Ile Leu Arg Leu Lys Glu Ser Ile Ala Ala Thr Asn Glu Ala Val
299          165          170          175
301 His Glu Val Thr Asp Gly Leu Ser Gln Leu Ala Val Ala Val Gly Lys
302          180          185          190
304 Met Gln Gln Phe Val Asn Asp Gln Phe Asn Lys Thr Ala Gln Glu Leu
305          195          200          205
307 Asp Cys Ile Lys Ile Ala Gln Gln Val Gly Val Glu Leu Asn Leu Tyr
308          210          215          220
310 Leu Thr Glu Ser Thr Thr Val Phe Gly Pro Gln Ile Thr Ser Pro Ala
311 225          230          235          240
313 Leu Asn Lys Leu Thr Ile Gln Ala Leu Tyr Asn Leu Ala Gly Gly Asn
314          245          250          255
316 Met Asp Tyr Leu Leu Thr Lys Leu Gly Ile Gly Asn Asn Gln Leu Ser
317          260          265          270
319 Ser Leu Ile Gly Ser Gly Leu Ile Thr Gly Asn Pro Ile Leu Tyr Asp
320          275          280          285
322 Ser Gln Thr Gln Leu Leu Gly Ile Gln Val Thr Leu Pro Ser Val Gly
323          290          295          300
325 Asn Leu Asn Asn Met Arg Ala Thr Tyr Leu Glu Thr Leu Ser Val Ser
326 305          310          315          320
328 Thr Thr Arg Gly Phe Ala Ser Ala Leu Val Pro Lys Val Val Thr Arg
329          325          330          335
331 Val Gly Ser Val Ile Glu Glu Leu Asp Thr Ser Tyr Cys Ile Glu Thr
332          340          345          350
334 Asp Leu Asp Leu Tyr Cys Thr Arg Ile Val Thr Phe Pro Met Ser Pro
335          355          360          365
337 Gly Ile Tyr Ser Cys Leu Ser Gly Asn Thr Ser Ala Cys Met Tyr Ser
338          370          375          380
340 Lys Thr Glu Gly Ala Leu Thr Thr Pro Tyr Met Thr Ile Lys Gly Ser
341 385          390          395          400
343 Val Ile Ala Asn Cys Lys Met Thr Thr Cys Arg Cys Val Asn Pro Pro
344          405          410          415
346 Gly Ile Ile Ser Gln Asn Tyr Gly Glu Ala Val Ser Leu Ile Asp Lys
347          420          425          430
349 Gln Ser Cys Asn Val Leu Ser Leu Gly Gly Ile Thr Leu Arg Leu Ser
350          435          440          445
352 Gly Glu Phe Asp Val Thr Tyr Gln Lys Asn Ile Ser Ile Gln Asp Ser
353          450          455          460
355 Gln Val Ile Ile Thr Gly Asn Leu Asp Ile Ser Thr Glu Leu Gly Asn
356 465          470          475          480
358 Val Asn Asn Ser Ile Ser Asn Ala Leu Asn Lys Leu Glu Glu Ser Asn
359          485          490          495

```

RAW SEQUENCE LISTING

DATE: 07/05/2001

PATENT APPLICATION: US/09/881,457

TIME: 11:30:02

Input Set : A:\SY01105K1QKQK Sequence Listing.txt

Output Set: N:\CRF3\07052001\I881457.raw

361 Arg Lys Leu Asp Lys Val Asn Val Lys Leu Thr Ser Thr Ser Ala Leu
362 500 505 510
364 Ile Thr Tyr Ile Val Leu Thr Ile Ile Ser Leu Val Phe Gly Ile Leu
365 515 520 525
367 Ser Leu Ile Leu Ala Cys Tyr Leu Met Tyr Lys Gln Lys Ala Gln Gln
368 530 535 540
370 Lys Thr Leu Leu Trp Leu Gly Asn Asn Thr Leu Asp Gln Met Arg Ala
371 545 550 555 560
373 Thr Thr Lys Met

F-11

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY

DATE: 07/05/2001

PATENT APPLICATION: US/09/881,457

TIME: 11:30:03

Input Set : A:\SY01105K1QKQK Sequence Listing.txt

Output Set: N:\CRF3\07052001\I881457.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:107 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:108 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:237 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:277 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:2
L:521 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:528 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:530 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:534 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:538 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:542 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:546 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:550 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:554 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:558 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:562 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:566 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:570 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:574 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:578 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:582 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:586 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:590 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:594 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:598 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:602 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:606 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:610 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:614 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:618 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3